IN THE CLAIMS

1. – 29. (cancelled)

30. (previously presented) A method of identifying a virus comprising:

contacting nucleic acid from said virus with at least one pair of primers which hybridize to flanking sequences of said nucleic acid, wherein said flanking sequences flank a variable nucleic acid sequence of said virus;

amplifying said variable nucleic acid sequence to produce an amplification product;

determining the base composition of said amplification product by mass spectrometry, wherein said base composition identifies the number of A residues, C residues, T residues, G residues, U residues, analogues thereof and mass tag residues thereof in said amplification product; and

comparing said base composition of said amplification product to calculated or measured base compositions of analogous amplification products of one or more known viruses present in a database comprising 5 or more base compositions with the proviso that sequencing of said amplification product is not used to identify the virus.

31. (previously presented) The method of claim 30, further comprising repeating said contacting, amplifying, determining and comparing steps using one or more additional pairs of primers.

32. (previously presented) The method of claim 30, wherein said virus is a biological warfare threat agent.

33. (previously presented) The method of claim 30, wherein said virus is identified at the sub-species level.

34 – 49. (cancelled).

50. (previously presented) The method of claim 30, wherein said virus is a respiratory pathogen.

51. (previously presented) The method of claim 30, wherein said virus is a hepatitis C virus.

52. (previously presented) The method of claim 30, wherein said virus in an immunodeficiency virus.

53. (currently amended) The method of claim 30, wherein said virus is a member of a viral family selected from the group consisting of *Filoviridae*, *Flavifiridae*, *Arenaviridae*, *Bunyaviridae*, *Adenoviridae*, *Picornaviridae*, *Togaviridae*, and *Coronoaviridae*.

54. (previously presented) The method of claim 56, wherein said housekeeping gene is a polymerase, a virion component, a helicase, a protease, a methyltransferase, or an accessory protein.

55. (previously presented) The method of claim 54, wherein said polymerase is RNA-dependent RNA polymerase, DNA-dependent DNA polymerase or DNA-dependent RNA polymerase.

56. (previously presented) The method of claim 30, wherein said nucleic acid is a housekeeping gene.

57. (previously presented) The method of claim 30, wherein said amplifying step comprises the polymerase chain reaction.

58. (previously presented) The method of claim 30, wherein the sequences to which the primers hybridize are separated by between about 60-100 nucleotides.

59. (previously presented) The method of claim 30, wherein said virus is identified at the species level.

60. (previously presented) The method of claim 30, wherein said pair of primers comprises at least one nucleotide analog.

61. (previously presented) The method of claim 60, wherein said nucleotide analog is inosine, uridine, 2.6-diaminopurine, propyne C, or propyne T.

62. (previously presented) The method of claim 30, wherein a molecular mass-modifying tag is incorporated into said amplification product to limit the number of possible base compositions consistent with the mass of said amplification product.